

FIG. 1

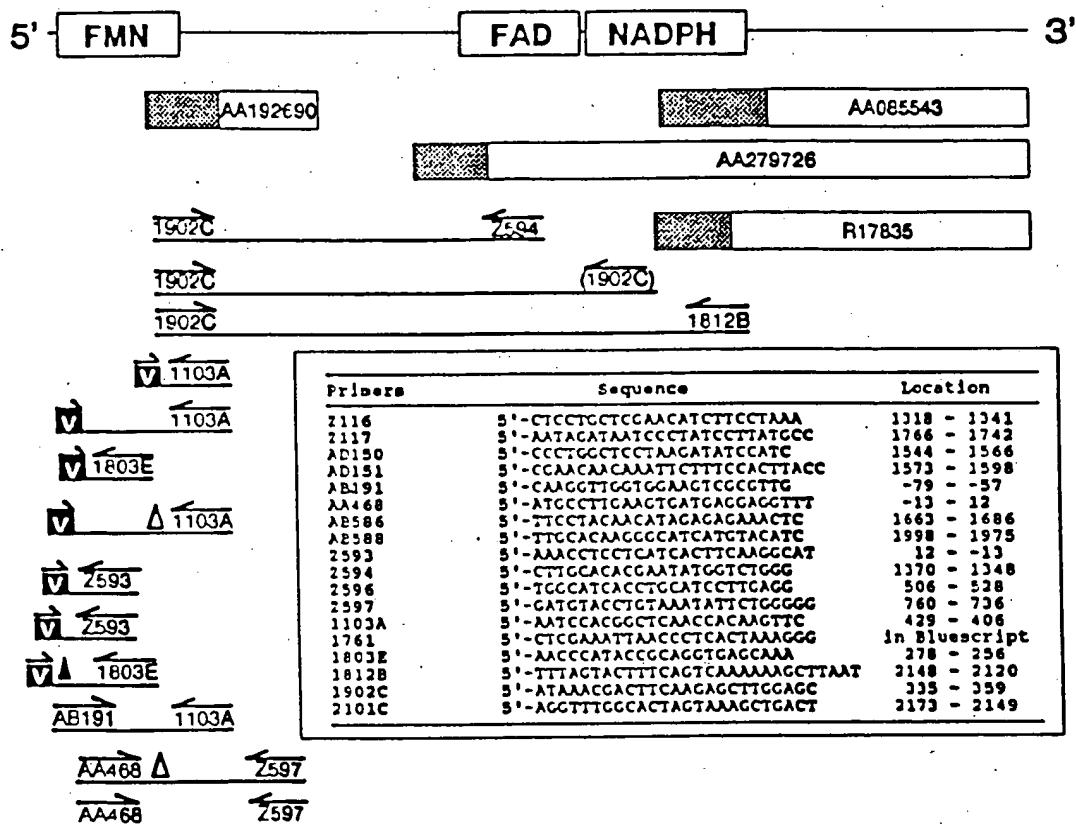


FIG. 2

1 ATGAGGAGGTTCTGTTACTATATGCTACACAGCAGGCACAGGCAAGGCCATCGCAAGAAATGTGTGAGCAAGCTGTTACATGATTCTGAA
 M R R F L L L Y A T O O G O A K A I A E E H C E Q A V V H G F S A O L H C I S E 40
 121 TCCGATAAGTATGACCTAAAACGCCAACCTCTCTCTGTTGTTTCTACACAGGCCACGGAGACCCACCCGACACGCCCAAGTTGTTAAGGAAATACAGAACAAACA
 S D K Y D L K T E T A P L V V V V S T T G T G D P P D T A R K F V K E I O N Q T 80
 241 CTGGGGTGTGATTCTCTGCTCACCTGGGTATGGTTACTGGGTCTGGTATTCAAGAATACACCTACTTTCAGAATGGGGGAAAGATAATGATAACAGCTTCAGGAGCC
 L P V D F F A H L R Y G L L G D S E Y T F C N G G K I I D K R L O E L G A 120
 361 CGGCAATTCTATGACACTGGACATGAGCTGTTAGGTTAGACTGTTGGCTGAGCTGGACTCTGGCAACCTCAGAAAGGATTTAGGTCAGGAGGACAA
 R H F Y D T G H A D D C V G L E L V V E P W I A G L W P A L R K H F R S S R G Q 160
 481 CAGGAGATAAGTGGGGCACTCCGGTGGCATCACCTGCATCTGGAGGACAGACCTGTAAGTCAGGCTGCTACACATTCAAGTCAGGCTCTGAGATTCGATGATTCAAGGA
 E E I S G A L P V A S P A S L R T D L V K S E L L R F D D S G 200
 601 AGAAAGGATTCTGAGGTTTCAAGAAAATCCAGTGAACAGCAACCAATCCATGTTCAATTGAGACTTTGAGTCTCACTTACCCCTGGTACCCCCACTCTCACAA
 R K D S E V L K O N A V N S N O S N V I E D F E S L T R S V P P L S O A S L 240
 721 AATATTCTGGTTACCCCAAGAAATTACAGGTACATCTGGAGGAGCTCTGGGAGGAAAGCCAAGTATCTGACTTCAGCAGATCCAGTTCAAGTGGCAATTCAAG
 N I P G L P P E Y L T V H L O E S L G O E E S O V S V T S A D P V F O V P I S K 280
 841 GCAGTCACACTACTACAGATGCTGATAAAACCCACTCTGCTGGTAGATTGGACATTTCAGCTGGAGATGCCCTACGGTGATCTGCCCTAACAGT
 A V O L T N D A I K T T L V E L D I S H T D F S Y O P G D A F S V I C P N S 320
 961 GATTCGAGGTACAAAGCTACTCCAAAGACTGGAGCTTGAAGATAAAAGGAGACACTGGCTCTTAAATAAAAGGCAACACAAAGAAGGAGCTACCTTACCCAGCATATA
 D S E V O S L L R D L O L E D K R E H C V L L K I K A D T K K G A T A L P O H I 360
 1081 CCTGGGGATGTTCTCCAGTTCTTACCTGGTCTGAAATCAGCAATTCTAAAGGCAATTCTGGAGCCCTTGTGGACTATACAGTGACAGTGTGAAAGGCCAGG
 P A G C S L O F I F T V C L E I R A I P K A F L R A L V D Y T S D S A E K R R 400
 1201 CTACAGGACTGTGAGTAAACAGGGCAGCGATTATAGCCGTTCTGAGGATGCTGTGCTGCTGATCTCTGCTGCTTCCCTCTGCTGAGCCACCCACTGCTC
 L O E L C S K O G A A D O Y S R F V R D A C A C L L D L L A F P S C O P P L S L 440
 1321 CTGGCTGAAACATCTCTAACCTAACCCAGACCATATTCGTTGCAAGCTCAAGTTATTACCCAGAAAGCTTCAACATTGAGTAACTCTGCTACTGGCACA
 C E H L P L O P R Y S C A S S L F H P G K L H F V H I V E F L S T A T 480
 1441 ACAGGGTTCTGGGAAGGGAGTATGACGGCTGGCTGGCTCTGGTTGCTTCAGTCTCAGGCAACATCATGAAACACAGGGAAAGCCCTGGCTCTAACAGATA
 T E V L R K G V C T G W L A L L V A S V L O P N I H A S H E D S G K A L A P K I 520
 1561 TCCATCTCTGGCAACAAACAACTTCTCACTTACAGATGACCCCTCAATCCCCTACATAATGGTGGGTCAGGAACCCGCTAGGCCCCTTATGGTCTCTAACACATAGAGAG
 S I S P R T T N S F H L P D P S I P I I M V G P G T G I A P F I G F L O H R E 560
 1681 AAACCTCAAGAACACACCCAGATGAAATTCTGAGCAATGCTGTTTGGCTGAGGCTAAAGGATAGGGATTATCTATTCAAGAAAAGAGCTCACATCTAACATGGG
 K L O E O H P D G N P D F F G C R H K D R D Y L F R K E L R H F L K H G 600
 1801 ATCTTAACCTCTAAAGGTTCTCTCAACAGATGCTCTGGGGAGGAGCCCAAGCAAGTATGACAAGAACATCCAGCTCATGGCCAGCAGTGGCAGAAATCTC
 I L T H L K V S F S R D A P V G E E E A P A K Y V O D N I O L H G O O V A R I L 640
 1921 TCCAGGAGAACGGCCATATTATGTTGCTGAGATGCAAGAAATATGCCAAGGATGACATGATGCCCTTGAGCAAAATAAAGCAAACAGGTTGGAGTTGAAAAACTAGAACGATG
 L O E N G H I Y V C G D A K N H D A L V O I S K E V G V E K L E A M 680
 2041 AAAACCTGGCCACTTAAAGAGAAAAACCTACCTTCAGGATATTGGCTATAAAACAGAAATTAAAGAGAGGATAAGCTTGTACTGAAGTACTAAAGTCAGCTTAC
 K T L A T L K E E K R Y T L O D I M S *** 698
 2161 TAGTGCCTAACCTTAAATTCAGGAAATTCTTCAACATTCTGAGGACATGGAGATTGGATCATTAAACATAAACAAAATCTCTGATTTGATTTACGTATC
 2281 TCTATCTACGCCCTCTGCTGCTGACTCTCCAAAATTGCCCTGCTGAGCTCTCTGAGCTAAAGGCCCTTCAGCTCTATCACGCCCTCTTACTCTCCAGAGAACT
 2401 TCACAGAGACTCTGCTCTCCATGAAAGGCTCTGAAATAGGGAGACTCACTGAGTAGCTCATTTCTGACTTACAGTGGCAACATTTAAAGATGAAAATGATTTTAA
 2521 TATGATGATACCCATAAACATGCTCATTTAAATGCAATTAAATACACATGAGGCTATCTGTTATGTAACTTCAATGGTATTTGTTACTAAAGCTATATTCTG
 2641 ATAAAAAAATTTAGGATAATGCTACAGGGATTATTTTATGCTGGGAAATATGAAATTTCACTGGGCTATGATTTTATCTACCCATTACCTT
 2761 TTTAAAGTCACAAATTCTGAGATTCTCCACATTATGCTCATTTACAGGTACCTGAGCTATTTAAAGAAAGATAACACCTTTTATTTCTACCTCTTATCTGCTGCTT
 2881 CCCACATTGGTGTGTTCTCCACATTATGCTCATGACCTCAAGGAGTGTGCTGGACCTAAAGACTGACTTTAGTGTAGTATCTTGGATTTAGATCTCCAGTGTCAA
 3001 TCCCTGTTATAATTGACAAAACAAACAAATTGATAATCTTCACTGTTCTAAATATATTGTATTTTATTTGATGCTGGGATTTAAACATCTGTTGAAGGCTT
 3121 TGATCTTTGAGAAATAAACATGAAAGAAATGGCTATAATCTAAAAA

FIG. 3 page 1 of 2

HsMTRR	-----		
CeMTRR	-----		
HsCPR	HGDSHVGTSSTVSEAVAEVSLFSMTDMILFLSLIVGLLTWFLFRKKKEE	50	
	FMN		
HsMTRR	-----MRFLLLYATGCCAKATAEENCE	24	
CeMTRR	-----MTOFLIAFCSCITCAETIAKSLKE	24	
HsCPR	VFEFTKIGTLTSSVRESSFVEKMKKTGRNIVFYGSGTGTAEFAHRLSK	100	
	FMN		
HsMTRR	CAVVCFCACLHC1SESDK-YDLKT-----ETAPLVVVVSTIGTCGPP	66	
CeMTRR	KAELIGLTFRLHALCENEKKFHLNE-----EXLC-AIVVSTGCGGAP	66	
HsCPR	DAHRTG----MRGMSADPEEYDLADLSSLPEDNAVLFCHMAYCEGOPT	146	
	FMN		
HsMTRR	CTAFLFVKEICHTLPVDOFFAHMLRIGLGLGCGSEYYTFCGGKTTICKRLD	116	
CeMTRR	ENCAFFVFRINRNSLENEYLKNLDYVLLGCGSNYSSYCTIFRKIDKLT	116	
HsCPR	DNACDDFYDULCETGVD---LSCGVKFAVFLGLCKTYEHFNAMGKRYVKRLE	193	
	FMN		
HsMTRR	ELGARHYDTCADDCVGLELVVEPWTIAGLWFLALRKHFPRSSRCOEISGA	166	
CeMTRR	ALGARLIGRAEADDCVGLEVEPWTIAKFLASRFDISADKHM----	162	
HsCPR	CLGACRIFELCIGCGCGNLEEDFTURECFWPAVCENF-----GV	233	
	FMN		
HsMTRR	LFVASPASLRDOLVKSELLHIESCVELL--RFDCSGRKESEVLKCHAVNS	214	
CeMTRR	-AITESENKLKNCVKTE---EKKALLCKRIDEEDESDDEGRGRVIGID-	206	
HsCPR	EAIEGEESSEFCYEL-----VVNTDIDAAKVYHGENGRKSTEN	271	
	FMN		
HsMTRR	NCNSNVVIEDF---ESSLTRSVPPPLS-CASLNIPGLPPEYLOVHLCESLCO	260	
CeMTRR	---MLTFEHYDYPEISSLKGSQTLNSDNLRVPIAPGPFLVSSVSNFKLP	253	
HsCPR	CKP-----FFD-----AKNPFLAAVTINRKL	293	
	FMN		
HsMTRR	EEECVS-----VTSADPVFCVP1SKAVOLTT--NDAIKTLLVELDIS	301	
CeMTRR	EDTXLEWCNLCKMPGVVTKFFEVLVSAEFV1DPSK1KTKRM17VDFG	303	
HsCPR	CGTE-----RNLMHLELD	306	
	FMN		
HsMTRR	N---TDFSTGFCAFSVICPNSDSEVCSLLQR-LOLEDKREHCVLLKIKAD	348	
CeMTRR	CHAAELCTEFCDAAITFCVFNPALENVFLIKRCVGVLIDAOOCCEL-SINPK	352	
HsCPR	ISCSK1RTESGCHAVYVPAANDSALVNOLGK---ILGADLD--VMSLHNLL	351	
	FMN		
HsMTRR	TKKKCATLPCNIPACCSLOFIFTUCLEIRAIPIKKAFLRALVDTTSDSAEK	398	
CeMTRR	TEKINACIFCHVHKITLFLHNNFTICLDIRAPGRPLIRVLAESTSDFNEK	402	
HsCPR	DEESENKXHF---/PCPTSYTIALTYLDITPPRTHVNLAYLACIASEFSEQ	399	
	FMN		
HsMTRR	RRPLOEL--CSKCGAACDYSRFVRDACA1LLDLLAFLPSCOPLSLLLEHLP	446	
CeMTRR	FRLLEL--CSACGMDHDFDFVRTPGCLSLADMLFAFPNVKPPVDRLLIELLP	450	
HsCPR	ELLRKPSSESGEGKELYLSVWVVEARRHILALI0OCPSLRFPIHLCLELP	449	
	FAD	FAD	FAD
HsMTRR	KLCFPTSCASSSLFHFGKLMHFVHNIVEFLSTATTEVLRKQVETGWLALL	496	
CeMTRR	FLTRPFYHSS---YENKXARLITSENEFPATDGRRRXRGLATDULNSL	497	
HsCPR	RLCARTYIASSSKVHPNSVHICAVVVEETKAGR--INKQVATNWL---	496	
	FAD	FAD	FAD
HsMTRR	VASVLOPNIHASHEDSGKALAKP11S1SPRTINSFHL-----DDPS1F	539	
CeMTRR	R-----1GDKV0VLCGEFARFLRPLPGMTKNSACKLP	529	
HsCPR	RAKE-----PVGENGGRALVPMFVRKS0FRLPK-----ATTIP	527	
	NADPH		
HsMTRR	1IMVPGTCIAFFIGFLCHREKLCOEONPQNGFMW-LFFGCRHKDRDTL	588	
CeMTRR	1LMVPGTCGVSVFSLFLHFLRKLCQDPSDSDVDPVRVLFFGCRROSSVDAI	579	
HsCPR	VIMVPGTCVAPPFIGF10ERAVLRCGGKE---VGETLLYTCCRSDEDYL	574	
	NADPH		
HsMTRR	FRKELRHFLXHGCLTMLKVSFSRDAFVGEEEAFAKYVODNIOLNGOCVAR	638	
CeMTRR	YHSELEMVFSEG11D11ICESEQ-----XGERVCDGLRKYLQKLP	621	
HsCPR	YREELACFHRDGAUTOLNVAFSRE---OSHKVYVOLLKQDREHNLW	618	
	NADPH		
HsMTRR	1LLOE-NGH1VCGOAKNNAKDVHDAVQ11SKEVGVEKLEAKTLATLK	687	
CeMTRR	FLTASTESK1FCCDAKGSKDQWCFSD1VASDOCIPDLEAKKLHDLK	671	
HsCPR	LI--EGGAH1VCGDARNHARDVONTFYD1VAELGAMEHACAVYTIKLM	666	
	NADPH/FAD		
HsMTRR	EKRYLQD1WS 698		
CeMTRR	KSDQYIEDWNG 682		
HsCPR	TKGRYLSDWWS 677		

HsMTRR	MGDGVDTSSVSEAVAEVLSFSMTDMILFLSLIVGLLTYWFLKKKKEL	50	
CeMTRR	-----MRRFLLLYATOOOGAAKAAEEMCE	24	
HsCPR	-----MTDFLIAFGSQTGOAETIAKSLKE	24	
	VPEFTKIOTLTSSVRESSFVEKMKKGRNIIIVFYGSQTGAEEFANRLSK	100	
	FMN		
HsMTRR	QAVVHGFSADLHCISESDK-YDLKT-----ETAPLVVVVSTTGTGDPP	66	
CeMTRR	KAELIGLTPTRLHALDENKKFNLNE-----EKLC-AIVVSTGTDGDP	66	
HsCPR	DAHRYG---MRGMSADPEEYDADLSSLPEIDNALVVFCMATYGEGLPT	146	
	***	***	
HsMTRR	DTARKFVKEIONQTLPVDFFAHLRYGLLGLGDSEYYFCNGGKIIDKRLQ	116	
CeMTRR	DNCARFVRRINRNSLENEYLKNLDYVLLGLGDSNYYOTIPRKIDKQLT	116	
HsCPR	DNAQDFYDWLQETDVD---LSGVKFAVFGLGNKTVEHFNAMGKYVVKRLE	193	
	***	***	
HsMTRR	ELGARHFYDTGHADDCVGLELVVEPIAGLWPALRKHFRRSSRGEEISGA	166	
CeMTRR	ALGANRLFDRAEADDOVGLLEVEPIWIEKFATLASRFDISADKMN---	162	
HsCPR	OLGAORIFELGLGDDGNLEEDF1TREOFWPACVEHF-----GV	233	
	***	***	
HsMTRR	LPVASPASLRTDLVKSSELLHIESOVELL--RFDDSGRKDSEVLKONAVNS	214	
CeMTRR	•AITESSNLKLNQVKTE---EKKALLOKRIEDEESDDEGRGRVIGID-	206	
HsCPR	EATGEESSIRQYEL-----VVHTDIDAQVYMGEMGRLKSYEN	271	
	***	***	
HsMTRR	NCSNVVIEDF---ESSLTRSVPPPLS-QASLNIPGLPPEYLOVHLOESLGQ	260	
CeMTRR	---MLIPEHYDYPEISLLKGSQLTSNDENLRVPIAOPFIVSSVSNRKL	253	
HsCPR	OKP-----PFD-----AKNPLAATTNRKLN	293	
	***	***	
HsMTRR	EESOVS-----VTSADPVFCVPISKAVOLTT--NDAIKTTLLVELDIS	301	
CeMTRR	EDTKLEWONLCKMPGVVTKPFEVLLVSAEFVTDPFSKKIKTRKMITVDFG	303	
HsCPR	OGTE-----RHLMHLELD	306	
	***	***	
HsMTRR	N--TDFSYOPGDAFSVICPNSDSEVQSLLQR-LOLEDKREHCVLLKIKAD	348	
CeMTRR	DHAAELOYEPGDAIYFCVPNPALEVNFILKRCGVLDIAOOCEL-SINPK	352	
HsCPR	ISDSKIRYESGDHVAVYVANDSALVNOLGK---ILGADL--VVMSLNLL	351	
	***	***	
HsMTRR	TKKKGATLPOHIPAGCSLOFIFTWCLEIRAIKPKAFLRALVDYTSDSAEK	398	
CeMTRR	TEKINAQIIPGHVHKITLRRHMFITCLDIRRAPGRPLIRVLAESTSDPNEK	402	
HsCPR	DEESNKKHP---FPCPTSYRTALTYLDITNPPRTNVLYELAQYASEPSEQ	399	
	***	***	
HsMTRR	RRLOEL--CSKOGAADYSRFVRDACAICLDDLLAFPSQOPPLSLLLEHLP	446	
CeMTRR	RRLEL--CSAGGMKDFTDVFVTPGLSLADMLFAFPNVKPPVDRLIELL	450	
HsCPR	ELLRKMASSSCEGKELYLSWWVARRHILAILODCPSLRRPPIDHLCLELL	449	
	***	***	
HsMTRR	FAD	FAD	FAD
CeMTRR	KLQPRPYSCASSSLFHPGKLHVFVNIVELSTATTEVLRKGVCWTGLALL	496	
HsCPR	RLIPRPySMSS---YENRKARLIYSEMEFPATDGRHSRKGLATDWLNSL	497	
	***	***	***
HsMTRR	RLOARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL--	494	
	***	***	***
HsMTRR	VASVLOPNIHASHEDSGKALAKPISIISPRITNSFHLP-----DDPSIP	539	
CeMTRR	R-----IGDKVOLGKEPARFRLPPLGMTNSAGKLP	529	
HsCPR	RAKE-----PVGENGGRALVPMFVRKSQFRLPFL-----ATTP	527	
	***	***	***
HsMTRR	NADPH		
CeMTRR	IIIVGPGTGIAPFIGFLQHREKLOEOPDGNFGAMW-LFFGCRHKORDYL	588	
HsCPR	LLMVGPGTGVSVFLSFLHFLRKLKODSPSDFVDPVRVLFFGCRDSSVDAI	579	
	***	***	***
HsMTRR	VIMVGPGBTGPVAFFIGF10ERAWLROOGKE---VGETLLYYGCRSDEDYL	574	
	***	***	***
HsMTRR	NADPH		NADPH
CeMTRR	FRKELRHFLKHGILTHLKVFSRDAVGEAEAPAKYVODNIOLHGQOVAR	638	
HsCPR	YMSSELEMFVSEGIITLDI1CESEO-----KGEROVODGLRKLYDKVLP	621	
	***	***	***
HsMTRR	YREELAQFHRDGALTOLNVAFSRE-----QSHKVYVCHLLKODREHLWK	618	
	***	***	***
HsMTRR	NADPH		
CeMTRR	ILLQE-NGHIYVCGDAKNMAKDVGHDALVQIISKEVGVEKLEAKTLATLK	687	
HsCPR	FLTASTESKIFIGCGDKGMSKDVWOCFSDIVASDOGIPDLEAKKLMIDLK	671	
	***	***	***
HsMTRR	L1--EGGAHIYVCGDARNMARDVONTFYDIVAELGAMEHAQAVDYIKKL	666	
	***	***	***
HsMTRR	NADPH/FAD		
CeMTRR	EEKRYLQDIWS 698		
HsCPR	KSDQYIEDVG 682		
	TKGRYSLDVS 677		

FIG. 4

FIG. 5A

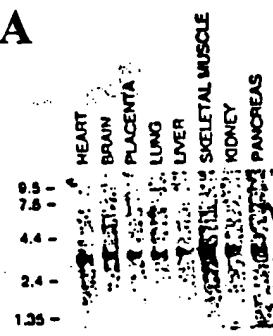


FIG. 5B



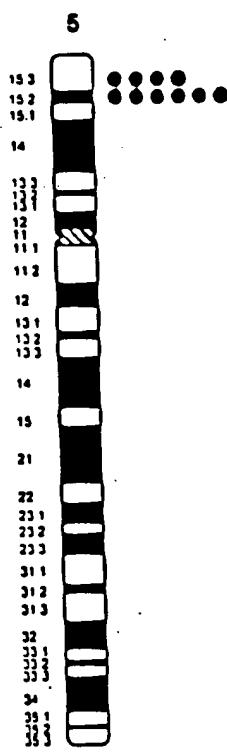


FIG. 6

FIG. 7A



FIG. 7B

FIG. 7C

Position	Sequence	Accessions	Protein	Organism
572	CAGVLTTCCHHPPDWVWLY	[AF025794]	WTBP	[H. sapiens]
598	CTTLLVYCCPSPDENTLY	[AAU557]	CPR	[H. sapiens]
599	CTTLLVYCCPRAAEDVLY	[D00101]	CPR	[O. cuniculus]
560	CTTLLVYCCPRAAEDVLY	[351490]	CPR	[D. melanogaster]
572	CTTLLVYCCPRAAEDVLY	[P37114]	CPR	[V. radiata]
573	CTTLLVYCCPRAAEDVLY	[226438]	CPR	[A. niger]
1281	CITVLLVFFCCPSPDENTLY	[D19408]	NOS	[H. sapiens]
1281	CITVLLVFFCCPSPDENTLY	[D09410]	NOS	[H. sapiens]
1009	CPNTLIVFCCPSPDENTLY	[U09410]	NOS	[H. sapiens]
1040	CPNTLIVFCCPSPDENTLY	[L26910]	NOS	[H. sapiens]
380	CPNTLIVFCCPSPDENTLY	[U09409]	NOS	[O. cuniculus]
1005	CDTLLVYCCPSPDENTLY	[U04408]	NOS	[O. cuniculus]
481	CPWLLVYCCPSPDENTLY	[M27408]	SP	[C. elegans]
915	CTTLLVYCCPSPDENTLY	[D26501]	SP	[S. cerevisiae]
407	CTTLLVYCCPSPDENTLY	[Z31149]	SP	[R. norvegicus]
241	CLAVLLVYCCPSPDENTLY	[X25417]	PRB	[P. sativus]
241	CLAVLLVYCCPSPDENTLY	[P00455]	PRB	[S. olaraceae]

FIG. 8A

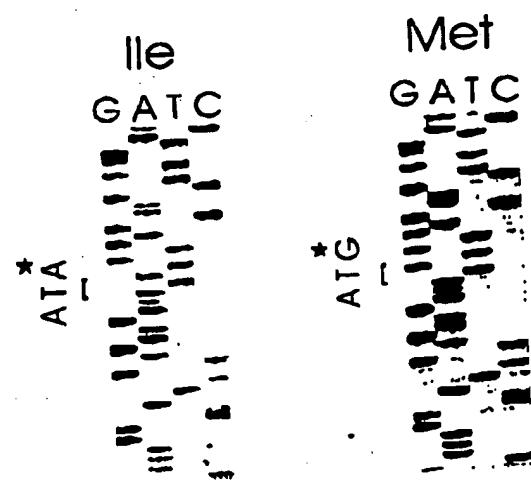


FIG. 8B

